

SEQUENCE LISTING

(1) GENERAL INFORMATION:



APPLICANTS:

Metz, James G.
Lardizabal, Kathryn D.
Lassner, Michael

TITLE OF INVENTION:

Nucleic Acid Sequences Encoding
a Plant Cytoplasmic Protein Involved in
Fatty Acyl-COA Metabolism

(iii) NUMBER OF SEQUENCES: 39

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Calgene, Inc.
- (B) STREET: 1920 Fifth Street
- (C) CITY: Davis
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 95616

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
- (B) COMPUTER: Apple Macintosh
- (C) OPERATING SYSTEM: Macintosh 7.0
- (D) SOFTWARE: Microsoft Word 5.1a

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US94/13686
- (B) FILING DATE: 30-NOV-94
- (C) CLASSIFICATION:

(vii) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/265,047
- (B) FILING DATE: 23-JUN-94
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/160,602
- (B) FILING DATE: 30-NOV-93
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/066,299
- (B) FILING DATE: 20-MAY-93

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US92/09863
- (B) FILING DATE: 13-NOV-92

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/933,411
- (B) FILING DATE: 21-AUG-92

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/796,256
- (B) FILING DATE: 20-NOV-91

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Donna E. Scherer
- (B) REGISTRATION NUMBER: 34,719
- (A) NAME: Carl J. Schwedler
- (B) REGISTRATION NUMBER: 36,924
- (C) REFERENCE/DOCKET NUMBER: CGNE 101-2 US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (916) 753-6313
- (B) TELEFAX: (916) 753-1510

(2) INFORMATION FOR SEQ ID NO: : 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAATCCTCCA CTCATACACT CCACCTCTCT CTCTCTCTGA AACAAATTGAA	60
GTAGCAAAC TAAAAGAAA ATG GAG GAA ATG GGA AGC ATT TTA GAG TTT CTT	112
Met Glu Glu Met Gly Ser Ile Leu Glu Phe Leu	
1 5 10	
GAT AAC AAA GCC ATT TTG GTC ACT GGT GCT ACT GGC TCC TTA GCA AAA	160
Asp Asn Lys Ala Ile Leu Val Thr Gly Ala Thr Gly Ser Leu Ala Lys	
15 20 25	
ATT TTT GTG GAG AAG GTA CTG AGG AGT CAA CCG AAT GTG AAG AAA CTC	208
Ile Phe Val Glu Lys Val Leu Arg Ser Gln Pro Asn Val Lys Lys Leu	
30 35 40	
TAT CTT CTT TTG AGA GCA ACC GAT GAC GAG ACA GCT GCT CTA CGC TTG	256
Tyr Leu Leu Leu Arg Ala Thr Asp Asp Glu Thr Ala Ala Leu Arg Leu	
45 50 55	
CAA AAT GAG GTT TTT GGA AAA GAG TTG TTC AAA GTT CTG AAA CAA AAT	304
Gln Asn Glu Val Phe Gly Lys Glu Leu Phe Lys Val Leu Lys Gln Asn	
60 65 70 75	
TTA GGT GCA AAT TTC TAT TCC TTT GTA TCA GAA AAA GTG ACT GTA GTA	352
Leu Gly Ala Asn Phe Tyr Ser Phe Val Ser Glu Lys Val Thr Val Val	
80 85 90	
CCC GGT GAT ATT ACT GGT GAA GAC TTG TGT CTC AAA GAC GTC AAT TTG	400
Pro Gly Asp Ile Thr Gly Glu Asp Leu Cys Leu Lys Asp Val Asn Leu	
95 100 105	
AAG GAA GAA ATG TGG AGG GAA ATC GAT GTT GTT GTC AAT CTA GCT GCT	448
Lys Glu Glu Met Trp Arg Glu Ile Asp Val Val Val Asn Leu Ala Ala	
110 115 120	

ACA ATC AAC TTC ATT GAA AGG TAC GAC GTG TCT CTG CTT ATC AAC ACA	496
Thr Ile Asn Phe Ile Glu Arg Tyr Asp Val Ser Leu Leu Ile Asn Thr	
125 130 135	
TAT GGA GCC AAG TAT GTT TTG GAC TTC GCG AAG AAG TGC AAC AAA TTA	544
Tyr Gly Ala Lys Tyr Val Leu Asp Phe Ala Lys Lys Cys Asn Lys Leu	
140 145 150 155	
AAG ATA TTT GTT CAT GTA TCT ACT GCT TAT GTA TCT GGA GAG AAA AAT	592
Lys Ile Phe Val His Val Ser Thr Ala Tyr Val Ser Gly Glu Lys Asn	
160 165 170	
GGG TTA ATA CTG GAG AAG CCT TAT TAT ATG GGC GAG TCA CTT AAT GGA	640
Gly Leu Ile Leu Glu Lys Pro Tyr Tyr Met Gly Glu Ser Leu Asn Gly	
175 180 185	
AGA TTA GGT CTG GAC ATT AAT GTA GAG AAG AAA CTT GTG GAG GCA AAA	688
Arg Leu Gly Leu Asp Ile Asn Val Glu Lys Lys Leu Val Glu Ala Lys	
190 195 200	
ATC AAT GAA CTT CAA GCA GCG GGG GCA ACG GAA AAG TCC ATT AAA TCG	736
Ile Asn Glu Leu Gln Ala Ala Gly Ala Thr Glu Lys Ser Ile Lys Ser	
205 210 215	
ACA ATG AAG GAC ATG GGC ATC GAG AGG GCA AGA CAC TGG GGA TGG CCA	784
Thr Met Lys Asp Met Gly Ile Glu Arg Ala Arg His Trp Gly Trp Pro	
220 225 230 235	
AAT GTG TAT GTA TTC ACC AAG GCA TTA GGG GAG ATG CTT TTG ATG CAA	832
Asn Val Tyr Val Phe Thr Lys Ala Leu Gly Glu Met Leu Leu Met Gln	
240 245 250	
TAC AAA GGG GAC ATT CCG CTT ACT ATT ATT CGT CCC ACC ATC ATC ACC	880
Tyr Lys Gly Asp Ile Pro Leu Thr Ile Ile Arg Pro Thr Ile Ile Thr	
255 260 265	
AGC ACT TTT AAA GAG CCC TTT CCT GGT TGG GTT GAA GGT GTC AGG ACC	928
Ser Thr Phe Lys Glu Pro Phe Pro Gly Trp Val Glu Gly Val Arg Thr	
270 275 280	
ATC GAT AAT GTA CCT GTA TAT TAT GGT AAA GGG AGA TTG AGG TGT ATG	976
Ile Asp Asn Val Pro Val Tyr Tyr Gly Lys Gly Arg Leu Arg Cys Met	
285 290 295	

CTT TGC GGA CCC AGC ACA ATA ATT GAC CTG ATA CCG GCA GAT ATG GTC Leu Cys Gly Pro Ser Thr Ile Ile Asp Leu Ile Pro Ala Asp Met Val 300 305 310 315	1024
GTG AAT GCA ACG ATA GTA GCC ATG GTG GCG CAC GCA AAC CAA AGA TAC Val Asn Ala Thr Ile Val Ala Met Val Ala His Ala Asn Gln Arg Tyr 320 325 330	1072
GTA GAG CCG GTG ACA TAC CAT GTG GGA TCT TCA GCG GCG AAT CCA ATG Val Glu Pro Val Thr Tyr His Val Gly Ser Ser Ala Ala Asn Pro Met 335 340 345	1120
AAA CTG AGT GCA TTA CCA GAG ATG GCA CAC CGT TAC TTC ACC AAG AAT Lys Leu Ser Ala Leu Pro Glu Met Ala His Arg Tyr Phe Thr Lys Asn 350 355 360	1168
CCA TGG ATC AAC CCG GAT CGC AAC CCA GTA CAT GTG GGT CGG GCT ATG Pro Trp Ile Asn Pro Asp Arg Asn Pro Val His Val Gly Arg Ala Met 365 370 375	1216
GTC TTC TCC TCC TTC TCC ACC TTC CAC CTT TAT CTC ACC CTT AAT TTC Val Phe Ser Ser Phe Ser Thr Phe His Leu Tyr Leu Thr Leu Asn Phe 380 385 390 395	1264
CTC CTT CCT TTG AAG GTA CTG GAG ATA GCA AAT ACA ATA TTC TGC CAA Leu Leu Pro Leu Lys Val Leu Glu Ile Ala Asn Thr Ile Phe Cys Gln 400 405 410	1312
TGG TTC AAG GGT AAG TAC ATG GAT CTT AAA AGG AAG ACG AGG TTG TTG Trp Phe Lys Gly Lys Tyr Met Asp Leu Lys Arg Lys Thr Arg Leu Leu 415 420 425	1360
TTG CGT TTA GTA GAC ATT TAT AAA CCC TAC CTC TTC TTC CAA GGC ATC Leu Arg Leu Val Asp Ile Tyr Lys Pro Tyr Leu Phe Phe Gln Gly Ile 430 435 440	1408
TTT GAT GAC ATG AAC ACT GAG AAG TTG CGG ATT GCT GCA AAA GAA AGC Phe Asp Asp Met Asn Thr Glu Lys Leu Arg Ile Ala Ala Lys Glu Ser 445 450 455	1456
ATA GTT GAA GCT GAT ATG TTT TAC TTT GAT CCC AGG GCA ATT AAC TGG Ile Val Glu Ala Asp Met Phe Tyr Phe Asp Pro Arg Ala Ile Asn Trp 460 465 470 475	1504

GAA GAT TAC TTC TTG AAA ACT CAT TTC CCA GGN GTC GTA GAG CAC GTT	1552
Glu Asp Tyr Phe Leu Lys Thr His Phe Pro Gly Val Val Glu His Val	
480	485
485	490
CTT AAC TAAAAGTTAC GGTACGAAAA TGAGAAGATT GGAATGCATG CACCGAAAGN	1608
Leu Asn	
NCAACATAAAA AGACGTGGTT AAAGTCATGG TCAAAAAAGA AATAAAATGC AGTTAGGTTT	1668
GTGTTGCAGT TTTGATTCCCT TGTATTGTTA CTTGTACTTT TGATCTTTTT CTCCCCAAT	1728
GAAATTCTC TCTTGTTT GTGAAAAAAA AAAAAAAA GAGCTCCTGC AGAAGCTT	1786

(2) INFORMATION FOR SEQ ID NO: 2 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2 :

GGAACCTCCAT CCCTTCCTCC CTCACTCCTC TCTCTACA ATG AAG GCC AAA ACA ATC	56
Met Lys Ala Lys Thr Ile	
1	5
ACA AAC CCG GAG ATC CAA GTC TCC ACG ACC ATG ACC ACC ACG ACC ACG	104
Thr Asn Pro Glu Ile Gln Val Ser Thr Thr Met Thr Thr Thr Thr Thr	
10	15
15	20
ACT ATG ACC GCC ACT CTC CCC AAC TTC AAG TCC TCC ATC AAC TTA CAC	152
Thr Met Thr Ala Thr Leu Pro Asn Phe Lys Ser Ser Ile Asn Leu His	
25	30
30	35
CAC GTC AAG CTC GGC TAC CAC TAC TTA ATC TCC AAT GCC CTC TTC CTC	200
His Val Lys Leu Gly Tyr His Tyr Leu Ile Ser Asn Ala Leu Phe Leu	
40	45
45	50

GTA	TTC	ATC	CCC	CTT	TTG	GGC	CTC	GCT	TCG	GCC	CAT	CTC	TCC	TCC	TTC		248
Val	Phe	Ile	Pro	Leu	Leu	Gly	Leu	Ala	Ser	Ala	His	Leu	Ser	Ser	Phe		
55				60						65					70		
TCG	GCC	CAT	GAC	TTG	TCC	CTG	CTC	TTC	GAC	CTC	CTT	CGC	CGC	AAC	CTC		296
Ser	Ala	His	Asp	Leu	Ser	Leu	Leu	Phe	Asp	Leu	Leu	Arg	Arg	Asn	Leu		
75					80							85					
CTC	CCT	GTT	GTC	GTT	TGT	TCT	TTC	CTC	TTC	GTT	TTA	TTA	GCA	ACC	CTA		344
Leu	Pro	Val	Val	Val	Cys	Ser	Phe	Leu	Phe	Val	Leu	Leu	Ala	Thr	Leu		
90						95					100						
CAT	TTC	TTG	ACC	CGG	CCC	AGG	AAT	GTC	TAC	TTG	GTG	GAC	TTT	GGA	TGC		392
His	Phe	Leu	Thr	Arg	Pro	Arg	Asn	Val	Tyr	Leu	Val	Asp	Phe	Gly	Cys		
105						110						115					
TAT	AAG	CCT	CAA	CCG	AAC	CTG	ATG	ACA	TCC	CAC	GAG	ATG	TTC	ATG	GAC		440
Tyr	Lys	Pro	Gln	Pro	Asn	Leu	Met	Thr	Ser	His	Glu	Met	Phe	Met	Asp		
120					125						130						
CGG	ACC	TCC	CGG	GCC	GGG	TCG	TTT	TCT	AAG	GAG	AAT	ATT	GAG	TTT	CAG		488
Arg	Thr	Ser	Arg	Ala	Gly	Ser	Phe	Ser	Lys	Glu	Asn	Ile	Glu	Phe	Gln		
135					140					145				150			
AGG	AAG	ATC	TTG	GAG	AGG	GCC	GGT	ATG	GGT	CGG	GAA	ACC	TAT	GTC	CCC		536
Arg	Lys	Ile	Leu	Glu	Arg	Ala	Gly	Met	Gly	Arg	Glu	Thr	Tyr	Val	Pro		
155						160						165					
GAA	TCC	GTC	ACT	AAG	GTG	CCC	GCC	GAG	CCG	AGC	ATA	GCA	GCA	GCC	AGG		584
Glu	Ser	Val	Thr	Lys	Val	Pro	Ala	Glu	Pro	Ser	Ile	Ala	Ala	Ala	Arg		
170						175						180					
GCC	GAG	GCG	GAG	GAG	GTG	ATG	TAC	GGG	GCG	ATC	GAC	GAG	GTG	TTG	GAG		632
Ala	Glu	Ala	Glu	Glu	Val	Met	Tyr	Gly	Ala	Ile	Asp	Glu	Val	Leu	Glu		
185						190						195					
AAG	ACG	GGG	GTG	AAG	CCG	AAG	CAG	ATA	GGA	ATA	CTG	GTG	GTG	ANC	TGC		680
Lys	Thr	Gly	Val	Lys	Pro	Lys	Gln	Ile	Gly	Ile	Leu	Val	Val	Xxx	Cys		
200						205						210					
AGC	TTG	TTT	AAC	CCA	ACG	CCG	TCG	CTG	TCA	TCC	ATG	ATA	GTT	AAC	CAT		728
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ser	Met	Ile	Val	Asn	His		
215						220					225			230			

TAC AAG CTN AGG GGT AAT ATA CTT AGC TAT AAT CTT GGT GGC ATG GGT Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly 235 240 245	776
TGC AGT GCT GGG CTC ATT TCC ATT GAT CTT GCC AAG GAC CTC CTA CAG Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu Ala Lys Asp Leu Leu Gln 250 255 260	824
GTT TAC CGT AAA AAC ACA TAT GTG TTA GTA GTG AGC ACG GAA AAC ATG Val Tyr Arg Lys Asn Thr Tyr Val Leu Val Val Ser Thr Glu Asn Met 265 270 275	872
ACC CTT AAT TGG TAC TGG GGC AAT GAC CGC TCC ATG CTT ATC ACC AAC Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser Met Leu Ile Thr Asn 280 285 290	920
TGC CTA TTT CGC ATG GGT GGC GCT GCC ATC ATC CTC TCA AAC CGC TGG Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile Leu Ser Asn Arg Trp 295 300 305 310	968
CGT GAT CGT CGC CGA TCC AAG TAC CAA CTC CTT CAT ACA GTA CGC ACC Arg Asp Arg Arg Ser Lys Tyr Gln Leu Leu His Thr Val Arg Thr 315 320 325	1016
CAC AAG GGC GCT GAC GAC AAG TCC TAT AGA TGC GTC TTA CAA CAA GAA His Lys Gly Ala Asp Asp Lys Ser Tyr Arg Cys Val Leu Gln Gln Glu 330 335 340	1064
GAT GAA AAT AAC AAG GTA GGT GTT GCC TTA TCC AAG GAT CTG ATG GCA Asp Glu Asn Asn Lys Val Gly Val Ala Leu Ser Lys Asp Leu Met Ala 345 350 355	1112
GTT GCC GGT GAA GCC CTA AAG GCC AAC ATC ACG ACC CTT GGT CCC CTC Val Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr Thr Leu Gly Pro Leu 360 365 370	1160
GTG CTC CCC ATG TCA GAA CAA CTC CTC TTC TTT GCC ACC TTA GTG GCA Val Leu Pro Met Ser Glu Gln Leu Leu Phe Phe Ala Thr Leu Val Ala 375 380 385 390	1208
CGT AAG GTC TTC AAG ATG ACG AAC GTG AAG CCA TAC ATC CCA GAT TTC Arg Lys Val Phe Lys Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe 395 400 405	1256

AAG TTG GCA GCG AAC GAC TTC TGC ATC CAT GCA GGA GGC AAA GCA GTG	1304																																																												
Lys Leu Ala Ala Asn Asp Phe Cys Ile His Ala Gly Gly Lys Ala Val																																																													
410	415	420		TTG GAT GAG CTC GAG AAG AAC TTG GAG TTG ACG CCA TGG CAC CTT GAA	1352	Leu Asp Glu Leu Glu Lys Asn Leu Glu Leu Thr Pro Trp His Leu Glu		425	430	435		CCC TCG AGG ATG ACA CTG TAT AGG TTT GGG AAC ACA TCG AGT AGC TCA	1400	Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn Thr Ser Ser Ser Ser		440	445	450		TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA GGG AGG ATC CGT AAG	1448	Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys Gly Arg Ile Arg Lys		455	460	465	470	GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA GGT TTC AAG TGT AAC	1496	Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn		475	480	485		AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT CCG GCT AGA GAG AAG	1544	Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys		490	495	500		AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA	1592	Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys		505	510	515		ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA	1640	Ile Ala Pro Ile Ala Ser		520		AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT	1700	CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG	1733
420																																																													
TTG GAT GAG CTC GAG AAG AAC TTG GAG TTG ACG CCA TGG CAC CTT GAA	1352																																																												
Leu Asp Glu Leu Glu Lys Asn Leu Glu Leu Thr Pro Trp His Leu Glu																																																													
425	430	435		CCC TCG AGG ATG ACA CTG TAT AGG TTT GGG AAC ACA TCG AGT AGC TCA	1400	Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn Thr Ser Ser Ser Ser		440	445	450		TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA GGG AGG ATC CGT AAG	1448	Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys Gly Arg Ile Arg Lys		455	460	465	470	GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA GGT TTC AAG TGT AAC	1496	Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn		475	480	485		AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT CCG GCT AGA GAG AAG	1544	Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys		490	495	500		AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA	1592	Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys		505	510	515		ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA	1640	Ile Ala Pro Ile Ala Ser		520		AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT	1700	CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG	1733								
435																																																													
CCC TCG AGG ATG ACA CTG TAT AGG TTT GGG AAC ACA TCG AGT AGC TCA	1400																																																												
Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn Thr Ser Ser Ser Ser																																																													
440	445	450		TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA GGG AGG ATC CGT AAG	1448	Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys Gly Arg Ile Arg Lys		455	460	465	470	GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA GGT TTC AAG TGT AAC	1496	Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn		475	480	485		AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT CCG GCT AGA GAG AAG	1544	Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys		490	495	500		AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA	1592	Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys		505	510	515		ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA	1640	Ile Ala Pro Ile Ala Ser		520		AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT	1700	CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG	1733																
450																																																													
TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA GGG AGG ATC CGT AAG	1448																																																												
Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys Gly Arg Ile Arg Lys																																																													
455	460	465	470	GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA GGT TTC AAG TGT AAC	1496	Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn		475	480	485		AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT CCG GCT AGA GAG AAG	1544	Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys		490	495	500		AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA	1592	Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys		505	510	515		ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA	1640	Ile Ala Pro Ile Ala Ser		520		AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT	1700	CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG	1733																								
465	470																																																												
GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA GGT TTC AAG TGT AAC	1496																																																												
Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser Gly Phe Lys Cys Asn																																																													
475	480	485		AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT CCG GCT AGA GAG AAG	1544	Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys		490	495	500		AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA	1592	Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys		505	510	515		ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA	1640	Ile Ala Pro Ile Ala Ser		520		AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT	1700	CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG	1733																																
485																																																													
AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT CCG GCT AGA GAG AAG	1544																																																												
Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn Pro Ala Arg Glu Lys																																																													
490	495	500		AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA	1592	Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys		505	510	515		ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA	1640	Ile Ala Pro Ile Ala Ser		520		AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT	1700	CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG	1733																																								
500																																																													
AAT CCT TGG ATG GAT GAA ATT GAG AAG TTC CCT GTC CAT GTG CCT AAA	1592																																																												
Asn Pro Trp Met Asp Glu Ile Glu Lys Phe Pro Val His Val Pro Lys																																																													
505	510	515		ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA	1640	Ile Ala Pro Ile Ala Ser		520		AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT	1700	CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG	1733																																																
515																																																													
ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT TAGTAATGAA	1640																																																												
Ile Ala Pro Ile Ala Ser																																																													
520																																																													
AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT GAGAACATGT	1700																																																												
CTCATTGAGA ATAACGTGTG CATCGTTGTG TTG	1733																																																												

(2) INFORMATION FOR SEQ ID NO:3 :

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3 :

GTCGACACA	ATG	AAG	GCC	AAA	ACA	ATC	ACA	AAC	CCG	GAG	ATC	CAA	GTC	TCC	51	
Met	Lys	Ala	Lys	Thr	Ile	Thr	Asn	Pro	Glu	Ile	Gln	Val	Ser			
1				5						10						
ACG	ACC	ATG	ACC	ACC	ACG	ACC	ACG	ACC	GCC	ACT	CTC	CCC	AAC	TTC	AAG	99
Thr	Thr	Met	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Thr	Leu	Pro	Asn	Phe	Lys	
15				20					25					30		
TCC	TCC	ATC	AAC	TTA	CAC	CAC	GTC	AAG	CTC	GGC	TAC	CAC	TAC	TTA	ATC	147
Ser	Ser	Ile	Asn	Leu	His	His	Val	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	
		35					40						45			
TCC	AAT	GCC	CTC	TTC	CTC	GTA	TTC	ATC	CCC	CTT	TTG	GGC	CTC	GCT	TCG	195
Ser	Asn	Ala	Leu	Phe	Leu	Val	Phe	Ile	Pro	Leu	Leu	Gly	Leu	Ala	Ser	
		50				55					60					
GCC	CAC	CTC	TCC	TCC	TTC	TCG	GCC	CAT	GAC	TTG	TCC	CTG	CTC	TTC	GAC	243
Ala	His	Leu	Ser	Ser	Phe	Ser	Ala	His	Asp	Leu	Ser	Leu	Leu	Phe	Asp	
		65				70					75					
CTC	CTT	CGC	CGC	AAC	CTC	CTC	CCC	GTT	GTC	GTT	TGT	TCT	TTC	CTC	TTC	291
Leu	Leu	Arg	Arg	Asn	Leu	Leu	Pro	Val	Val	Val	Cys	Ser	Phe	Leu	Phe	
		80				85					90					
GTT	TTA	TTA	GCA	ACC	CTA	CAT	TTC	TTG	ACC	CGG	CCT	AGG	AAT	GTC	TAC	339
Val	Leu	Leu	Ala	Thr	Leu	His	Phe	Leu	Thr	Arg	Pro	Arg	Asn	Val	Tyr	
		95				100			105					110		
TTG	GTG	GAC	TTT	GCC	TGC	TAT	AAG	CCT	CAC	CCG	AAC	CTG	ATA	ACA	TCC	387
Leu	Val	Asp	Phe	Ala	Cys	Tyr	Lys	Pro	His	Pro	Asn	Leu	Ile	Thr	Ser	
		115					120						125			
CAC	GAG	ATG	TTC	ATG	GAC	CGG	ACC	TCC	CGG	GCC	GGG	TCG	TTT	TCT	AAG	435
His	Glu	Met	Phe	Met	Asp	Arg	Thr	Ser	Arg	Ala	Gly	Ser	Phe	Ser	Lys	
		130				135						140				
GAG	AAT	ATT	GAG	TTT	CAG	AGG	AAG	ATC	TTG	GAG	AGG	GCC	GGT	ATG	GGC	483
Glu	Asn	Ile	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Glu	Arg	Ala	Gly	Met	Gly	
		145				150					155					

CGG GAA ACC TAC GTC CCC GAA TCC GTC ACT AAG GTG CCG CCC GAG CCG	Arg Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Val Pro Pro Glu Pro	531	
160	165	170	
AGC ATA GCA GCA GCC AGG GCC GAG GCG GAG GAG GTG ATG TAC GGG GCG	Ser Ile Ala Ala Ala Arg Ala Glu Ala Glu Glu Val Met Tyr Gly Ala	579	
175	180	185	190
ATC GAC GAG GTG TTG GAG AAG ACG GGG GTG AAG CCG AAG CAG ATA GGA	Ile Asp Glu Val Leu Glu Lys Thr Gly Val Lys Pro Lys Gln Ile Gly	627	
195	200	205	
ATA CTG GTG GTG AAC TGC AGC TTG TTT AAC CCA ACG CCG TCG CTG TCA	Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser	675	
210	215	220	
TCC ATG ATA GTT AAC CAT TAC AAG CTT AGG GGT AAT ATA CTT AGC TAT	Ser Met Ile Val Asn His Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr	723	
225	230	235	
AAT CTT GGT GGC ATG GGT TGC AGT GCT GGG CTC ATT TCC ATT GAT CTT	Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu	771	
240	245	250	
GCC AAG GAC CTC CTA CAG GTT TAC CGT AAC ACA TAT GTG TTA GTA GTG	Ala Lys Asp Leu Leu Gln Val Tyr Arg Asn Thr Tyr Val Leu Val Val	819	
255	260	265	270
AGC ACA GAA AAC ATG ACC CTT AAT TGG TAC TGG GGC AAT GAC CGC TCC	Ser Thr Glu Asn Met Thr Leu Asn Trp Tyr Trp Gly Asn Asp Arg Ser	867	
275	280	285	
ATG CTT ATC ACC AAC TGC CTA TTT CGC ATG GGT GGC GCT GCC ATC ATC	Met Leu Ile Thr Asn Cys Leu Phe Arg Met Gly Gly Ala Ala Ile Ile	915	
290	295	300	
CTC TCA AAC CGC TGG CGT GAT CGT CGC CGA TCC AAG TAC CAA CTC CTT	Leu Ser Asn Arg Trp Arg Asp Arg Arg Ser Lys Tyr Gln Leu Leu	963	
305	310	315	
CAC ACA GTA CGC ACC CAC AAG GGC GCT GAC GAC AAG TCC TAT AGA TGC	His Thr Val Arg Thr His Lys Gly Ala Asp Asp Lys Ser Tyr Arg Cys	1011	
320	325	330	

GTC TTA CAA CAA GAA GAT GAA AAT AAC AAG GTA GGT GTT GCC TTA TCC		1059
Val Leu Gln Gln Glu Asp Glu Asn Asn Lys Val Gly Val Ala Leu Ser		
335	340	345
350		
AAG GAT CTG ATG GCA GTT GCC GGT GAA GCC CTA AAG GCC AAC ATC ACG		1107
Lys Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys Ala Asn Ile Thr		
355	360	365
ACC CTT GGT CCC CTC GTG CTC CCC ATG TCA GAA CAA CTC CTC TTC TTT		1155
Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu Leu Phe Phe		
370	375	380
GCC ACC TTA GTG GCA CGT AAG GTC TTC AAG ATG ACG AAC GTG AAG CCA		1203
Ala Thr Leu Val Ala Arg Lys Val Phe Lys Met Thr Asn Val Lys Pro		
385	390	395
TAC ATC CCA GAT TTC AAG TTG GCA GCG AAG CAC TTC TGC ATC CAT GCA		1251
Tyr Ile Pro Asp Phe Lys Leu Ala Ala Lys His Phe Cys Ile His Ala		
400	405	410
GGA GGC AAA GCA GTG TTG GAT GAG CTC GAG ACG AAC TTG GAG TTG ACG		1299
Gly Gly Lys Ala Val Leu Asp Glu Leu Glu Thr Asn Leu Glu Leu Thr		
415	420	425
430		
CCA TGG CAC CTT GAA CCC TCG AGG ATG ACA CTG TAT AGG TTT GGG AAC		1347
Pro Trp His Leu Glu Pro Ser Arg Met Thr Leu Tyr Arg Phe Gly Asn		
435	440	445
ACA TCG AGT AGC TCA TTA TGG TAC GAG TTG GCA TAC GCT GAA GCA AAA		1395
Thr Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ala Glu Ala Lys		
450	455	460
GGG AGG ATC CGT AAG GGT GAT CGA ACT TGG ATG ATT GGA TTT GGT TCA		1443
Gly Arg Ile Arg Lys Gly Asp Arg Thr Trp Met Ile Gly Phe Gly Ser		
465	470	475
GGT TTC AAG TGT AAC AGT GTT GTG TGG AGG GCT TTG AGG AGT GTC AAT		1491
Gly Phe Lys Cys Asn Ser Val Val Trp Arg Ala Leu Arg Ser Val Asn		
480	485	490
CCG GCT AGA GAG AAG AAT CCT TGG ATG GAT GAA ATT GAG AAT TTC CCT		1539
Pro Ala Arg Glu Lys Asn Pro Trp Met Asp Glu Ile Glu Asn Phe Pro		
495	500	505
		510

GTC CAT GTG CCT AAA ATC GCA CCT ATC GCT TCG TAGAACTGCT AGGATGTGAT 1592
Val His Val Pro Lys Ile Ala Pro Ile Ala Ser
515 520

TAGTAATGAA AAATGTGTAT TATGTTAGTG ATGTAGAAAA AGAAACTTTA GTTGATGGGT 1652
GAGAACATGT CTCATTGAGA ATAACGTGTG CATCGTTGTG TTGAATTGAA ATTTGAGTAT 1712
TGGTGAAATT CTGTTAGAAT TGACGCATGA GTCATATATA TACAAATTAA AGTAAGATT 1772
TACGCTTTCT T 1783

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: PCR to genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4 :

GGCGCGCCGG TACCTCTAGA CCTGGCGATT CAACGTGGTC GGATCATGAC GCTTCCAGAA 60

AACATCGAGC AAGCTCTCAA AGCTGACCTC TTTCGGATCG TACTGAACCC GAACAATCTC 120

GTTATGTCCC GTCGTCTCCG AACAGACATC CTCGTAGCTC GGATTATCGA CGAATCCATG 180

GCTATACCCA ACCTCCGTCT TCGTCACGCC TGGAACCCCTC TGGTACGCCA ATTCCGCTCC 240

CCAGAAGCAA CCGGCGCCGA ATTGCGCGAA TTGCTGACCT GGAGACGGAA CATCGTCGTC 300

GGGTCCCTTGC GCGATTGCGG CGGAAGCCGG GTCGGGTTGG GGACGAGACC CGAATCCGAG 360

CCTGGTGAAG AGGTTGTTCA TCGGAGATTT ATAGACGGAG ATGGATCGAG CGGTTTGAG 420

GAAAGGGGAA GTGGGTTTGG CTCTTTGGA TAGAGAGAGT GCAGCTTGG AGAGAGACTG 480

GAGAGGTTA GAGAGAGACG CGGCGGATAT TACCGGAGGA GAGGCGACGA GAGATAGCAT 540

TATCGAAGGG	GAGGGAGAAA	GAGTGACGTG	GAGAAATAAG	AAACCGTTAA	GAGTCGGATA	600
TTTATCATAT	TAAAAGCCCA	ATGGGCCTGA	ACCCATTAA	ACAAGACAGA	TAAATGGGCC	660
GTGTGTTAAG	TTAACAGAGT	GTAAACGTTC	GGTTCAAAT	GCCAACGCCA	TAGGAACAAA	720
ACAAACGTGT	CCTCAAGTAA	ACCCCTGCCG	TTTACACCTC	AATGGCTGCA	TGGTGAAGCC	780
ATTAACACGT	GGCGTAGGAT	GCATGACGAC	GCCATTGACA	CCTGACTCTC	TTCCCTTCTC	840
TTCATATATC	TCTAATCAAT	TCAACTACTC	ATTGTCATAG	CTATTGGAA	AATACATACA	900
CATCCTTTTC	TCTTCGATCT	CTCTCAATT	ACAAGAAGCA	AAGTCGACGG	ATCCCTGCAG	960
TAAATTACGC	CATGACTATT	TTCATAGTCC	AATAAGGCTG	ATGTCGGGAG	TCCAGTTTAT	1020
GAGCAATAAG	GTGTTTAGAA	TTTGATCAAT	GTAAAGGCTG	ATGTCGGGAG	TCCAGTTTAT	1080
CAGTCTTTG	TTCTTTTGG	CTTTGTTAA	ATTGTCGTGT	TTCTATTGT	AAACCTCCTG	1140
TATATGTTGT	ACTTCTTCC	CTTTTAAGT	GGTATCGTCT	ATATGGTAAA	ACGTTATGTT	1200
TGGTCTTC	TTTCTCTGT	TTAGGATAAA	AAGACTGCAT	GTAAAGGCTG	TAGTTATATT	1260
ATGTTGAGTA	AATGAACCTT	CATAGATCTG	GTTCCGTAGA	GTAGACTAGC	AGCCGAGCTG	1320
AGCTGAACTG	AACAGCTGGC	AATGTGAACA	CTGGATGCAA	GATCAGATGT	GAAGATCTCT	1380
AATATGGTGG	TGGGATTGAA	CATATCGTGT	CTATATTTT	GTTGGCATT	AGCTCTTAAC	1440
ATAGATATAA	CTGATGCAGT	CATTGGTTCA	TACACATATA	TAGTAAGGAA	TTACAATGGC	1500
AACCCAAACT	TCAAAAACAG	TAGGCCACCT	GAATTGCCTT	ATCGAATAAG	AGTTTGTTC	1560

CCCCCACTTC ATGGGATGTA ATACATGGGA TTTGGGAGTT TGAATGAACG TTGAGACATG 1620

GCAGAACCTC TAGAGGTACC GGCGCGC 1647

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5 :

Glu Thr Tyr Val Pro Glu Ser Val Thr Lys Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6 :

Val Pro Xaa Glu Pro Ser Ile Ala Ala Xaa
5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :

Glu Thr Tyr Val Pro Glu Glu Val Thr Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8 :

Asp Leu Met Ala Val Ala Gly Glu Ala Leu Lys
5 10

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9 :

Met Thr Asn Val Lys Pro Tyr Ile Pro Asp Phe
5 10

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10 :

Phe Leu Pro Xaa Xaa Val Ala Ile Thr Gly Glu
5 10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

Phe Gly Asn Thr Ser Ser Xaa Xaa Leu Tyr Xaa Glu Leu Ala Tyr Ala
5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12 :

Ala Glu Ala Glu Glu Val Met Tyr Gly Ala Ile Asp Glu Val Leu Glu
5 10 15
Lys

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 residues

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13 :

Xaa Asp Ile Ala Ile Ile Gly Ser Gly Ser Ala Gly Leu Ala Gln Ala
5 10 15

Xaa Ile Leu Lys Asp Ala Gly
20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14 :

Gln Gln Phe Thr Val Trp Xaa Asn Ala Ser Glu Pro Ser
5 10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15 :

AAYATHACNA CNYTNGG

17

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16 :

SWRTTRCAYT TRAANCC

17

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17 :

GAA ATG AGT AGG TCT AGC GAA CAA GAT CTA CTC TCT ACC GAG ATT GTT
Met Ser Arg Ser Ser Glu Gln Asp Leu Leu Ser Thr Glu Ile Val
1 5 10 15

48

AAC CGT GGG ATC GAA CCT TCC GGT CCA AAC GCC GGT TCA CCA ACG TTC
Asn Arg Gly Ile Glu Pro Ser Gly Pro Asn Ala Gly Ser Pro Thr Phe
20 25 30

96

TCG GTC AGA GTC CGG AGA CGT TTA CCG GAT TTT CTT CAA TCC GTA AAC
Ser Val Arg Val Arg Arg Leu Pro Asp Phe Leu Gln Ser Val Asn
35 40 45

144

TTG AAG TAC GTG AAA CTT GGT TAT CAC TAC CTC ATA AAC CAT GCG GTT Leu Lys Tyr Val Lys Leu Gly Tyr His Tyr Leu Ile Asn His Ala Val 50 55 60	192
TAC TTG GCG ACG ATA CCG GTT CTT GTG CTT GTG TTT AGT GCC GAA GTT Tyr Leu Ala Thr Ile Pro Val Leu Val Leu Val Phe Ser Ala Glu Val 65 70 75	240
GGG AGT TTA AGC GGA GAA GAG ATT TGG AAG AAG CTT TGG GAC TAT GAT Gly Ser Leu Ser Gly Glu Glu Ile Trp Lys Lys Leu Trp Asp Tyr Asp 80 85 90 95	288
ATC GCA ACC GTC ATC GGA TTC TTC GGT GTC TTT GTC TTG ACC GTT TGC Ile Ala Thr Val Ile Gly Phe Phe Gly Val Phe Val Leu Thr Val Cys 100 105 110	336
GTC TAC TTC ATG TCT CGT CCA CGA TCT GTT TAT CTC ATT GAC TTC GCT Val Tyr Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Ile Asp Phe Ala 115 120 125	384
TGT TTC AAG CCT TCC GAT GAA CTT AAG GTG ACA AGA GAA GAG TTC ATA Cys Phe Lys Pro Ser Asp Glu Leu Lys Val Thr Arg Glu Glu Phe Ile 130 135 140	432
GAT CTA GCT AGA AAA TCA GGC AAG TTC GAC GAA GAG ATC CTC GGA TTC Asp Leu Ala Arg Lys Ser Gly Lys Phe Asp Glu Glu Ile Leu Gly Phe 145 150 155	480
AAG AAG AGG ATC CTT CAA GCC TCA GGA ATA GGC GAT GAA ACG TAC GTC Lys Lys Arg Ile Leu Gln Ala Ser Gly Ile Gly Asp Glu Thr Tyr Val 160 165 170 175	528
CCA AGA TCA ATC TCT TCG TCG GAA AAC ACA ACA ACG ATG AAA GAA GGT Pro Arg Ser Ile Ser Ser Glu Asn Thr Thr Met Lys Glu Gly 180 185 190	576
CGT GAA GAA GCC TCG ATG ATG ATA TTC GGC GCA CTC GAC GAA CTC TTC Arg Glu Glu Ala Ser Met Met Ile Phe Gly Ala Leu Asp Glu Leu Phe 195 200 205	624
GAG AAG ACA CGT GTC AAA CCG AAA GAC GTA GGT GTC CTC GTG GTT AAC Glu Lys Thr Arg Val Lys Pro Lys Asp Val Gly Val Leu Val Val Asn 210 215 220	672

TGC	AGT	ATC	TTT	AAC	CCG	ACT	CCG	TCA	CTC	TCC	GCG	ATG	GTG	ATT	AAC	720
Cys	Ser	Ile	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Ile	Asn	
225							230					235				
CAC	TAC	AAG	ATG	AGA	GGG	AAC	ATA	CTT	AGC	TAC	AAC	CTA	GGA	GGG	ATG	768
His	Tyr	Lys	Met	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn	Leu	Gly	Gly	Met	
240						245				250			255			
GGT	TGC	TCA	GCA	GGA	ATC	ATA	GCC	GTT	GAT	CTT	GCT	CGT	GAC	ATG	CTT	816
Gly	Cys	Ser	Ala	Gly	Ile	Ile	Ala	Val	Asp	Leu	Ala	Arg	Asp	Met	Leu	
						260			265			270				
CAG	TCT	AAC	CCG	AAT	AGT	TAC	GCG	GTG	GTT	GTG	AGT	ACC	GAG	ATG	GTT	864
Gln	Ser	Asn	Pro	Asn	Ser	Tyr	Ala	Val	Val	Val	Ser	Thr	Glu	Met	Val	
275							280				285					
GGG	TAT	AAT	TGG	TAC	GTG	GGA	CGT	GAC	AAG	TCA	ATG	GTT	ATA	CCT	AAC	912
Gly	Tyr	Asn	Trp	Tyr	Val	Gly	Arg	Asp	Lys	Ser	Met	Val	Ile	Pro	Asn	
290						295					300					
TGC	TTC	TTT	AGG	ATG	GGT	TGC	TCC	GCC	GTT	ATG	CTG	TCT	AAC	CGC	CGC	960
Cys	Phe	Phe	Arg	Met	Gly	Cys	Ser	Ala	Val	Met	Leu	Ser	Asn	Arg	Arg	
305						310					315					
CGT	GAC	TTC	CGC	CAT	GCT	AAG	TAC	CGC	CTT	GAG	CAC	ATT	GTC	CGG	ACT	1008
Arg	Asp	Phe	Arg	His	Ala	Lys	Tyr	Arg	Leu	Glu	His	Ile	Val	Arg	Thr	
320						325				330			335			
CAC	AAG	GCT	GCC	GAC	GAC	CGT	AGC	TTC	AGG	AGT	GTG	TAC	CAG	GAA	GAA	1056
His	Lys	Ala	Ala	Asp	Asp	Arg	Ser	Phe	Arg	Ser	Val	Tyr	Gln	Glu	Glu	
						340				345			350			
GAT	GAA	CAA	GGA	TTC	AAG	GGA	TTA	AAA	ATA	AGC	AGA	GAC	CTA	ATG	GAA	1104
Asp	Glu	Gln	Gly	Phe	Lys	Gly	Leu	Lys	Ile	Ser	Arg	Asp	Leu	Met	Glu	
						355			360			365				
GTT	GGA	GGT	GAA	GCT	CTC	AAG	ACC	AAC	ATC	ACC	ACC	TTA	GGC	CCT	CTC	1152
Val	Gly	Gly	Glu	Ala	Leu	Lys	Thr	Asn	Ile	Thr	Thr	Leu	Gly	Pro	Leu	
						370			375			380				
GTC	CTT	CCT	TTC	TCC	GAG	CAG	CTT	CTC	TTC	TTT	GCC	GCT	TTG	ATC	CGT	1200
Val	Leu	Pro	Phe	Ser	Glu	Gln	Leu	Leu	Phe	Phe	Ala	Ala	Leu	Ile	Arg	
						385			390			395				

AGA ACT TTC TCA CCC GCC AAA ACT ACC ACC ACC TCC TCC TCA GCC	1248
Arg Thr Phe Ser Pro Ala Ala Lys Thr Thr Thr Ser Ser Ser Ala	
400 405 410 415	
ACT GCG AAA ATC AAC GGA GCC AAG TCG TCA TCC TCC TCT GAT CTA TCC	1296
Thr Ala Lys Ile Asn Gly Ala Lys Ser Ser Ser Ser Ser Asp Leu Ser	
420 425 430	
AAG CCG TAC ATC CCG GAC TAC AAG CTT GCC TTC GAG CAT TTC TGC TTC	1344
Lys Pro Tyr Ile Pro Asp Tyr Lys Leu Ala Phe Glu His Phe Cys Phe	
435 440 445	
CAC GCG GCA AGC AAA GCG GTG CTT GAG GAG CTT CAG AAG AAT CTA GGC	1392
His Ala Ala Ser Lys Ala Val Leu Glu Glu Leu Gln Lys Asn Leu Gly	
450 455 460	
TTG AGT GAT GAG AAC ATG GAG GCT TCT AAG ATG ACT TTA CAC AGG TTT	1440
Leu Ser Asp Glu Asn Met Glu Ala Ser Lys Met Thr Leu His Arg Phe	
465 470 475	
GGA AAC ACT TCC AGC AGT GGA ATC TGG TAC GAG CTT GCT TAC ATG GAG	1488
Gly Asn Thr Ser Ser Gly Ile Trp Tyr Glu Leu Ala Tyr Met Glu	
480 485 490 495	
GCC AAG GAG AGT GTT CGT AGA GGC GAT AGG GTT TGG CAG ATT GCT TTT	1536
Ala Lys Glu Ser Val Arg Arg Gly Asp Arg Val Trp Gln Ile Ala Phe	
500 505 510	
GGG TCA GGT TTT AAG TGT AAC AGT GTG GTT TGG AAG GCA ATG AGG AAG	1584
Gly Ser Gly Phe Lys Cys Asn Ser Val Val Trp Lys Ala Met Arg Lys	
515 520 525	
GTG AAG AAG CCG GCA AGG AAC AAT CCT TGG GTT GAT TGC ATT AAC CGT	1632
Val Lys Lys Pro Ala Arg Asn Asn Pro Trp Val Asp Cys Ile Asn Arg	
530 535 540	
TAC CCT GTC GCT CTC TGATCATTTA TTTTTAAAAT TATTATTCT TCTTAATTAA	1687
Tyr Pro Val Ala Leu	
545	
ATCATCTATG ATCTCTCTTC CTTGTTGTTG GATGATAGAC GTTTGTTGC TGGTCATTG 1747	
TATCTTAAGA CTTCTATAAG AATGGATGGT TCAAGTCCAA AAAAAAAA AAAAAAAA 1807	
AAA	1810

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18 :

GTCGACAAA ATG ACG TCC ATT AAC GTA AAG CTC CTT TAC CAT TAC GTC ATA 51
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile
1 5 10

ACC AAC CTT TTC AAC CTT TGT TTC TTT CCA TTA ACG GCG ATC GTC GCC 99
Thr Asn Leu Phe Asn Leu Cys Phe Pro Leu Thr Ala Ile Val Ala
15 20 25 30

GGA AAA GCC TAT CGG CTT ACC ATA GAC GAT CTT CAC CAC TTA TAC TAT 147
Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr
35 40 45

TCC TAT CTC CAA CAC AAC CTC ATA ACC ATT GCT CCA CTC TTT GCC TTC 195
Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe
50 55 60

ACC GTT TTC GGT TCG GTT CTC TAC ATC GCA ACC CGG CCC AAA CCG GTT 243
Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val
65 70 75

TAC CTC GTT GAG TAC TCA TGC TAC CTT CCA CCA ACG CAT TGT AGA TCA 291
Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser
80 85 90

AGT ATC TCC AAG GTC ATG GAT ATC TTT TAC CAA GTA AGA AAA GCT GAT 339
Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp
95 100 105 110

CCT TCT CGG AAC GGC ACG TGC GAT GAC TCG TCC TGG CTT GAC TTC TTG	387
Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu	
115 120 125	
AGG AAG ATT CAA GAA CGT TCA GGT CTA GGC GAT GAA ACC CAC GGG CCC	435
Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro	
130 135 140	
GAG GGG CTG CTT CAG GTC CCT CCC CGG AAG ACT TTT GCG GCG GCG CGT	483
Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg	
145 150 155	
GAA GAG ACG GAG CAA GTT ATC ATT GGT GCG CTA GAA AAT CTA TTC AAG	531
Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys	
160 165 170	
AAC ACC AAT GTT AAC CCT AAA GAT ATA GGT ATA CTT GTG GTG AAC TCA	579
Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser	
175 180 185 190	
AGC ATG TTT AAT CCA ACT CCT TCG CTC TCC GCG ATG GTC GTT AAC ACT	627
Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr	
195 200 205	
TTC AAG CTC CGA AGC AAC GTA AGA AGC TTT AAC CTT GGT GGC ATG GGT	675
Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly	
210 215 220	
TGT AGT GCC GGC GTT ATA GCC ATT GAT CTA GCA AAG GAC TTG TTG CAT	723
Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His	
225 230 235	
GTC CAT AAA AAT ACG TAT GCT CTT GTG GTG AGC ACA GAG AAC ATC ACT	771
Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr	
240 245 250	
TAT AAC ATT TAC GCT GGT GAT AAT AGG TCC ATG ATG GTT TCA AAT TGC	819
Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys	
255 260 265 270	
TTG TTC CGT GTT GGT GGG GCC GCT ATT TTG CTC TCC AAC AAG CCT AGA	867
Leu Phe Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg	
275 280 285	

GAT	CGT	AGA	CGG	TCC	AAG	TAC	GAG	CTA	GTT	CAC	ACG	GTT	CGA	ACG	CAT	915
Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	
290								295					300			
ACC	GGA	GCT	GAC	GAC	AAG	TCT	TTT	CGT	TGC	GTG	CAA	CAA	GGA	GAC	GTT	963
Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Val	
305						310					315					
GAG	AAC	GGC	AAA	ACC	GGA	GTG	AGT	TTG	TCC	AAG	GAC	ATA	ACC	GAT	GTT	1011
Glu	Asn	Gly	Lys	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	
320					325					330						
GCT	GGT	CGA	ACG	GTT	AAG	AAA	AAC	ATA	GCA	ACG	CTG	GGT	CCG	TTG	ATT	1059
Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	
335					340					345			350			
CTT	CCG	TTA	AGC	GAG	AAA	CTT	CTT	TTT	TTC	GTT	ACC	TTC	ATG	GGC	AAG	1107
Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	
355								360					365			
AAA	CTT	TTC	AAA	GAC	AAA	ATC	AAA	CAT	TAT	TAC	GTC	CCG	GAC	TTC	AAG	1155
Lys	Leu	Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	
370								375					380			
CTT	GCT	ATC	GAC	CAT	TTT	TGT	ATA	CAT	GCC	GGA	GGC	AAA	GCC	GTG	ATT	1203
Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Lys	Ala	Val	Ile	
385							390					395				
GAT	GTG	CTA	GAG	AAG	AAC	CTA	GGC	CTA	GCA	CCG	ATC	GAT	GTA	GAG	GCA	1251
Asp	Val	Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	
400					405						410					
TCA	AGA	TCA	ACG	TTA	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCT	AGC	TCA	ATA	1299
Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	
415						420					425			430		
TGG	TAT	GAG	TTG	GCA	TAC	ATA	GAA	GCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT	1347
Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	
					435					440			445			
AAT	AAA	GTT	TGG	CAG	ATT	GCT	TTA	GGG	TCA	GGC	TTT	AAG	TGT	AAC	AGT	1395
Asn	Lys	Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	
450								455					460			

GCA GTT TGG GTG GCT CTA AAC AAT GTC AAA GCT TCC AAA TAGGATCC	1442
Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser Lys	
465	470
	475

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19 :

GTTCGACAAA ATG ACG TCC ATT AAC GTA AAG CTC CTT TAC CAT TAC GTC ATA	51
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile	
1	5
	10

ACC AAC CTT TTC AAC CTT TGC TTC TTT CCG TTA ACG GCG ATC GTC GCC	99
Thr Asn Leu Phe Asn Leu Cys Phe Pro Leu Thr Ala Ile Val Ala	
15	20
	25
	30

GGA AAA GCC TAT CGG CTT ACC ATA GAC GAT CTT CAC CAC TTA TAC TAT	147
Gly Lys Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr	
35	40
	45

TCC TAT CTC CAA CAC AAC CTC ATA ACC ATC GCT CCA CTC TTT GCC TTC	195
Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe	
50	55
	60

ACC GTT TTC GGT TCG GTT CTC TAC ATC GCA ACC CGG CCC AAA CCG GTT	243
Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val	
65	70
	75

TAC CTC GTT GAG TAC TCA TGC TAC CTT CCA CCA ACG CAT TGT AGA TCA	291
Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser	
80	85
	90

AGT ATC TCC AAG GTC ATG GAT ATC TTT TAT CAA GTC AGA AAA GCT GAT		339	
Ser Ile Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp			
95	100	105	110
CCT TCT CGG AAC GGC ACG TGC GAT GAC TCG TCG TGG CTT GAC TTC TTG		387	
Pro Ser Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu			
115	120	125	
AGG AAG ATT CAA GAA CGT TCA GGT CTA GGC GAT GAA ACT CAC GGG CCC		435	
Arg Lys Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro			
130	135	140	
GAG GGG CTG CTT CAG GTC CCT CCC CGG AAG ACT TTT GCG GCG GCG CGT		483	
Glu Gly Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg			
145	150	155	
GAA GAG ACG GAG CAA GTT ATC ATT GGT GCG CTA GAA AAT CTA TTC AAG		531	
Glu Glu Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys			
160	165	170	
AAC ACC AAC GTT AAC CCT AAA GAT ATA GGT ATA CTT GTG GTG AAC TCA		579	
Asn Thr Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser			
175	180	185	190
AGC ATG TTT AAT CCA ACT CCA TCG CTC TCC GCG ATG GTC GTT AAC ACT		627	
Ser Met Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr			
195	200	205	
TTC AAG CTC CGA AGC AAC GTA AGA AGC TTT AAC CTT GGT GGC ATG GGT		675	
Phe Lys Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly			
210	215	220	
TGT AGT GCC GGC GTT ATA GCC ATT GAT CTA GCA AAG GAC TTG TTG CAT		723	
Cys Ser Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His			
225	230	235	
GTC CAT AAA AAT ACG TAT GCT CTT GTG GTG AGC ACA GAG AAC ATC ACT		771	
Val His Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr			
240	245	250	
TAT AAC ATT TAC GCT GGT GAT AAT AGG TCC ATG ATG GTT TCA AAT TGC		819	
Tyr Asn Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys			
255	260	265	270

TTG	TTC	CGT	GTT	GGT	GGG	GCC	GCT	ATT	TTG	CTC	TCC	AAC	AAG	CCT	GGA		867
Leu	Phe	Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly		
				275					280					285			
GAT	CGT	AGA	CGG	TCC	AAG	TAC	GAG	CTA	GTT	CAC	ACG	GTT	CGA	ACG	CAT		915
Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His		
				290				295				300					
ACC	GGA	GCT	GAC	GAC	AAG	TCT	TTT	CGT	TGC	GTG	CAA	CAA	GGA	GAC	GAT		963
Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp		
				305			310				315						
GAG	AAC	GGC	AAA	ATC	GGA	GTG	AGT	TTG	TCC	AAG	GAC	ATA	ACC	GAT	GTT		1011
Glu	Asn	Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val		
				320			325			330							
GCT	GGT	CGA	ACG	GTT	AAG	AAA	AAC	ATA	GCA	ACG	TTG	GGT	CCG	TTG	ATT		1059
Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile		
				335			340			345				350			
CTT	CCG	TTA	AGC	GAG	AAA	CTT	CTT	TTT	TTC	GTT	ACC	TTC	ATG	GGC	AAG		1107
Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys		
				355				360			365						
AAA	CTT	TTC	AAA	GAT	AAA	ATC	AAA	CAT	TAC	TAC	GTC	CCG	GAT	TTC	AAA		1155
Lys	Leu	Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys		
				370				375					380				
CTT	GCT	ATT	GAC	CAT	TTT	TGT	ATA	CAT	GCC	GGA	GGC	AGA	GCC	GTG	ATT		1203
Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile		
				385			390			395							
GAT	GTG	CTA	GAG	AAG	AAC	CTA	GCC	CTA	GCA	CCG	ATC	GAT	GTA	GAG	GCA		1251
Asp	Val	Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala		
				400			405				410						
TCA	AGA	TCA	ACG	TTA	CAT	AGA	TTT	GGA	AAC	ACT	TCA	TCT	AGC	TCA	ATA		1299
Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile		
				415			420			425				430			
TGG	TAT	GAG	TTG	GCA	TAC	ATA	GAA	GCA	AAA	GGA	AGG	ATG	AAG	AAA	GGT		1347
Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly		
				435				440			445						

AAT AAA GTT TGG CAG ATT GCT TTA GGG TCA GGC TTT AAG TGT AAC AGT 1395
Asn Lys Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser
450 455 460

GCA GTT TGG GTG GCT CTA AAC AAT GTC AAA GCT TCC AAA TAGGATCC 1442
Ala Val Trp Val Ala Leu Asn Asn Val Lys Ala Ser Lys
465 470 475

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20 :

AAG CTT AAA CTA GTG TAT CAT TAC CTA ATC TCC AAC GCT CTC TAC ATC 48
Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Leu Tyr Ile
1 5 10 15

CTC CTC CTT CCT CTC CTC GCC GCA ACA ATC GCT AAC CTC TCT TCT TTC 96
Leu Leu Leu Pro Leu Leu Ala Ala Thr Ile Ala Asn Leu Ser Ser Phe
20 25 30

ACC ATC AAC GAC CTC TCT CTC CTC TAC AAC ACA CTC CGT TTC CAT TTC 144
Thr Ile Asn Asp Leu Ser Leu Leu Tyr Asn Thr Leu Arg Phe His Phe
35 40 45

CTC TCC GCC ACA CTC GCC ACC GCA CTC TTG ATC TCT CTC TCC ACC GCT 192
Leu Ser Ala Thr Leu Ala Thr Ala Leu Leu Ile Ser Leu Ser Thr Ala
50 55 60

TAC TTC ACC ACC CGT CCT CGC CGT GTC TTC CTC CTC GAC TTC TCG TGT 240
Tyr Phe Thr Thr Arg Pro Arg Arg Val Phe Leu Leu Asp Phe Ser Cys
65 70 75 80

TAC AAA CCA GAC CCT TCA CTG ATC TGC ACT CGT GAA ACA TTC ATG GAC	288
Tyr Lys Pro Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp	
85	90
95	
AGA TCT CAA CGT GTA GGC ATC TTC ACA GAA GAC AAC TTA GCT TTC CAA	336
Arg Ser Gln Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln	
100	105
110	
CAA AAG ATC CTC GAA AGA TCC GGT CTA GGT CAG AAA ACT TAC TTC CCT	384
Gln Lys Ile Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro	
115	120
125	
GAA GCT CTT CTT CGT GTT CCT CCT AAT CCT TGT ATG GAA GAA GCG AGA	432
Glu Ala Leu Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg	
130	135
140	
AAA GAG GCA GAA ACA GTT ATG TTC GGA GCT ATT GAC GCG GTT CTT GAG	480
Lys Glu Ala Glu Thr Val Met Phe Gly Ala Ile Asp Ala Val Leu Glu	
145	150
155	160
AAG ACC GGT GTG AAA CCT AAA GAT ATT GGA ATC CTT GTG GTG AAT TGT	528
Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys	
165	170
175	
AGC TTG TTT AAT CCA ACA CCG TCA CTT TCT GCT ATG ATT GTG AAT AAG	576
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys	
180	185
190	
TAT AAG CTT AGA GGC AAC ATT TTG AGC TAT AAT TTC GGC GGG ATG GG	623
Tyr Lys Leu Arg Gly Asn Ile Leu Ser Tyr Asn Phe Gly Gly Met Gly	
195	200
205	

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21 :

AAG	CTT	AAG	TTA	GGC	TAC	CAC	TAT	CTG	ATC	ACT	CAC	TTT	TTT	AAA	CTC	48
Lys		Leu	Lys	Leu	Gly	Tyr	His	Tyr	Leu	Ile	Thr	His	Phe	Phe	Lys	Leu
1					5					10					15	
ATG	TTC	CTC	CCT	CTA	ATG	GCT	GTT	TTG	TTC	ATG	AAT	GTC	TCA	TTG	TTA	96
Met	Phe	Leu	Pro	Leu	Met	Ala	Val	Leu	Phe	Met	Asn	Val	Ser	Leu	Leu	
					20				25				30			
AGC	CTA	AAC	CAT	CTT	CAG	CTC	TAT	TAC	AAT	TCC	ACC	GGA	TTC	ATC	TTC	144
Ser	Leu	Asn	His	Leu	Gln	Leu	Tyr	Tyr	Asn	Ser	Thr	Gly	Phe	Ile	Phe	
					35				40			45				
GTC	ATC	ACT	CTC	GCC	ATT	GTC	GGA	TCC	ATT	GTC	TTC	TTC	ATG	TCT	CGA	192
Val	Ile	Thr	Leu	Ala	Ile	Val	Gly	Ser	Ile	Val	Phe	Phe	Met	Ser	Arg	
					50		55			60						
CCT	AGA	TCC	ATC	TAC	CTT	CTA	GAT	TAC	TCT	TGC	TAC	CTC	CCG	CCT	TCG	240
Pro	Arg	Ser	Ile	Tyr	Leu	Leu	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Ser	
					65		70		75			80				
AGT	CAA	AAA	GTT	AGC	TAC	CAG	AAA	TTC	ATG	AAC	AAC	TCT	AGT	TTG	ATT	288
Ser	Gln	Lys	Val	Ser	Tyr	Gln	Lys	Phe	Met	Asn	Asn	Ser	Ser	Leu	Ile	
					85			90				95				
CAA	GAT	TTC	AGC	GAA	ACT	TCT	CTT	GAG	TTC	CAG	AGG	AAG	ATC	TTG	ATT	336
Gln	Asp	Phe	Ser	Glu	Thr	Ser	Leu	Glu	Phe	Gln	Arg	Lys	Ile	Leu	Ile	
					100			105			110					
CGC	TCT	GGT	CTC	GGT	GAA	GAG	ACT	TAT	TTA	CCG	GAT	TCT	ATT	CAC	TCT	384
Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	Asp	Ser	Ile	His	Ser	
					115			120			125					
ATC	CCT	CCG	CGT	CCT	ACT	ATG	GCT	GCA	GCG	CGT	GAA	GAA	GCG	GAG	CAG	432
Ile	Pro	Pro	Arg	Pro	Thr	Met	Ala	Ala	Ala	Arg	Glu	Glu	Ala	Glu	Gln	
					130		135			140						
GTA	ATC	TTC	GGT	GCA	CTC	GAC	AAT	CTT	TTC	GAG	AAT	ACA	AAA	ATC	AAT	480
Val	Ile	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	Glu	Asn	Thr	Lys	Ile	Asn	
					145		150		155			160				

CCT AGG GAG ATT GGT GTT CTT GTG AAT TGT AGT TTG TTT AAC CCC 528
Pro Arg Glu Ile Gly Val Leu Val Val Asn Cys Ser Leu Phe Asn Pro
165 170 175

ACG CCT TCT TTA TCC GCC ATG ATT GTT AAC AAG TAT AAG CTT AGA GGA 576
Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly
180 185 190

AAC ATT AAG AGC TTT AAT CTC GGC GGC ATG G 607
Asn Ile Lys Ser Phe Asn Leu Gly Gly Met
195 200

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAG CTT AAA CTG GGG TAC CAC TAC CTC ATT ACT CAT CTC TTC AAG CTC 48
Lys Leu Lys Leu Gly Tyr His Tyr Leu Ile Thr His Leu Phe Lys Leu
1 5 10 15

TGT TTG GTT CCA TTA ATG GCG GTT TTA GTC ACA GAG ATC TCC CGA TTA 96
Cys Leu Val Pro Leu Met Ala Val Leu Val Thr Glu Ile Ser Arg Leu
20 25 30

ACA ACA GAC GAT CTT TAC CAG ATT TGC CTT CAT CTC CAA TAC AAT CTC 144
Thr Thr Asp Asp Leu Tyr Gln Ile Cys Leu His Leu Gln Tyr Asn Leu
35 40 45

GTT GCT TTC ATC TTT CTC TCT GCT TTA GCT ATC TTT GGC TCC ACC GTT 192
Val Ala Phe Ile Phe Leu Ser Ala Leu Ala Ile Phe Gly Ser Thr Val
50 55 60

TAC	ATC	ATG	AGT	CGT	CCC	AGA	TCT	GTT	TAT	CTC	GTT	GAT	TAC	TCT	TGT	240
Tyr	Ile	Met	Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Val	Asp	Tyr	Ser	Cys	
65					70				75						80	
TAT	CTT	CCT	CCG	GAG	AGT	CTT	CAG	GTT	AAG	TAT	CAG	AAG	TTT	ATG	GAT	288
Tyr	Leu	Pro	Pro	Glu	Ser	Leu	Gln	Val	Lys	Tyr	Gln	Lys	Phe	Met	Asp	
85								90						95		
CAT	TCT	AAG	TTG	ATT	GAA	GAT	TTC	AAT	GAG	TCA	TCT	TTA	GAG	TTT	CAG	336
His	Ser	Lys	Leu	Ile	Glu	Asp	Phe	Asn	Glu	Ser	Ser	Leu	Glu	Phe	Gln	
			100					105						110		
AGG	AAG	ATT	CTT	GAA	CGT	TCT	GGT	TTA	GGA	GAA	GAG	ACT	TAT	CTC	CCT	384
Arg	Lys	Ile	Leu	Glu	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	
			115				120					125				
GAA	GCT	TTA	CAT	TGT	ATC	CCT	CCG	AGG	CCT	ACG	ATG	ATG	GCG	GCT	CGT	432
Glu	Ala	Leu	His	Cys	Ile	Pro	Pro	Arg	Pro	Thr	Met	Met	Ala	Ala	Arg	
			130				135				140					
GAG	GAA	GCT	GAG	CAG	GTA	ATG	TTT	GGT	GCT	CTT	GAT	AAG	CTT	TTC	GAG	480
Glu	Glu	Ala	Glu	Gln	Val	Met	Phe	Gly	Ala	Leu	Asp	Lys	Leu	Phe	Glu	
			145			150			155				160			
AAT	ACC	AAG	ATT	AAC	CCT	AGG	GAT	ATT	GGT	GTG	TTG	GTT	GTG	AAT	TGT	528
Asn	Thr	Lys	Ile	Asn	Pro	Arg	Asp	Ile	Gly	Val	Leu	Val	Val	Asn	Cys	
					165				170				175			
AGC	TTG	TTT	AAT	CCT	ACA	CCT	TCG	TTG	TCA	GCT	ATG	ATT	GTT	AAC	AAG	576
Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	
					180			185				190				
TAT	AAG	CTT	AGA	GGG	AAT	GTT	AAG	AGT	TTT	AAC	CTG	GGG	GGC	ATT	G	622
Tyr	Lys	Leu	Arg	Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Ile		
			195				200				205					

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23 :

AAG CTT AAG TTA TGG TAT CAC TAC CTG ATT TCT CAC CTT TTT AAG CTC Lys Leu Lys Leu Trp Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu 1 5 10 15	48
TTG TTG GTT CCT TTA ATG GCG GTT CTG TTC ACG AAT GTC TCC CGG TTA Leu Leu Val Pro Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu 20 25 30	96
AGC CTA AAC CAG CTC TGT CTC GAT CTC TCT CTC CAG CTC CAG TTC AAT Ser Leu Asn Gln Leu Cys Leu Asp Leu Ser Leu Gln Leu Gln Phe Asn 35 40 45	144
CTC GTC GGA TTC ATC TTC ATT ACC GTC TCC ATT TTC GGA TTC ACA Leu Val Gly Phe Ile Phe Ile Thr Val Ser Ile Phe Gly Phe Thr 50 55 60	192
GTT ATC TTC ATG TCC CGA CCT AGA TCC GTT TAC CTC CTC GAC TAC TCA Val Ile Phe Met Ser Arg Pro Arg Ser Val Tyr Leu Leu Asp Tyr Ser 65 70 75 80	240
TGT TAC CTC CCG CCG TCG AAT CTC AAA GTT AGC TAC CAG ACA TTC ATG Cys Tyr Leu Pro Pro Ser Asn Leu Lys Val Ser Tyr Gln Thr Phe Met 85 90 95	288
AAT CAT TCT AAA CTG ATT GAA GAT TTC GAC GAG TCG TCG CTT GAG TTC Asn His Ser Lys Leu Ile Glu Asp Phe Asp Glu Ser Ser Leu Glu Phe 100 105 110	336
CAG CGG AAG ATC CTG AAG CGA TCC GGT CTC GGC GAA GAG ACT TAC CTC Gln Arg Lys Ile Leu Lys Arg Ser Gly Leu Gly Glu Thr Tyr Leu 115 120 125	384
CCG GAA TCT ATC CAC TGC ATC CCG CCG CGT CCG ACT ATG GCG GCG GCG Pro Glu Ser Ile His Cys Ile Pro Pro Arg Pro Thr Met Ala Ala Ala 130 135 140	432
CGT GAG GAA TCG GAG CAG GTA ATC TTC GGT GCA CTC GAC AAT CTC TTC Arg Glu Glu Ser Glu Gln Val Ile Phe Gly Ala Leu Asp Asn Leu Phe 145 150 155 160	480

GAG AAT ACC AAA ATC GAC CCT AGG GAG ATT GGT GTT GTG GTG AAC	528
Glu Asn Thr Lys Ile Asp Pro Arg Glu Ile Gly Val Val Val Val Asn	
165	170
	175
TGC AGC TTG TTT AAC CCG ACG CCT TCT TTA TCC GCC ATG ATT GTG AAC	576
Cys Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn	
180	185
	190
AAG TAT AAG CTT AGA GGA AAC GTG AAG AGC TTT AAT CTC GGT GGC ATG G	625
Lys Tyr Lys Leu Arg Gly Asn Val Lys Ser Phe Asn Leu Gly Gly Met	
195	200
	205

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTTCATTGAT TTGTTTGAGA CTCTGTTGCA GAAATCTCCA C ATG GAT GAT GAA TCC	56
Met Asp Asp Glu Ser	
1	5
GTT AAT GGA GGA TCC GTA CAG ATC CGG ACC CGA AAG TAC GTC AAG CTG	104
Val Asn Gly Gly Ser Val Gln Ile Arg Thr Arg Lys Tyr Val Lys Leu	
10	15
	20
GGT TAT CAC TAC CTG ATT TCT CAC CTT TTT AAG CTC TTG TTG GTT CCT	152
Gly Tyr His Tyr Leu Ile Ser His Leu Phe Lys Leu Leu Leu Val Pro	
25	30
	35
TTA ATG GCG GTT CTG TTC ACG AAT GTC TCC CGG TTA AGC CTA AAC CAG	200
Leu Met Ala Val Leu Phe Thr Asn Val Ser Arg Leu Ser Leu Asn Gln	
40	45
	50

CTC	TGT	CTC	GAT	CTC	TCT	CTC	CAG	CTC	CAG	TTC	AAT	CTC	GTC	GGA	TTC		248
Leu	Cys	Leu	Asp	Leu	Ser	Leu	Gln	Leu	Gln	Phe	Asn	Leu	Val	Gly	Phe		
55						60								65			
ATC	TTC	TTC	ATT	ACC	GCC	TCC	ATT	TTC	GGA	TTC	ACA	GTT	ATC	TTC	ATG		296
Ile	Phe	Phe	Ile	Thr	Ala	Ser	Ile	Phe	Gly	Phe	Thr	Val	Ile	Phe	Met		
70						75				80				85			
TCC	CGA	CCT	AGA	TCC	GTT	TAC	CTC	CTC	GAC	TAC	TCA	TGT	TAC	CTC	CCG		344
Ser	Arg	Pro	Arg	Ser	Val	Tyr	Leu	Leu	Asp	Tyr	Ser	Cys	Tyr	Leu	Pro		
						90			95				100				
NCG	GCG	AAT	CTC	AAA	GTT	AGC	TAC	CAG	ACA	TTC	ATG	AAT	CAT	TCT	AAA		392
Xxx	Ala	Asn	Leu	Lys	Val	Ser	Tyr	Gln	Thr	Phe	Met	Asn	His	Ser	Lys		
						105			110				115				
CTG	ATT	GAA	GAT	TTC	GAC	GAG	TCG	TCG	CTT	GAG	TTC	CAG	CGG	AAG	ATC		440
Leu	Ile	Glu	Asp	Phe	Asp	Glu	Ser	Ser	Leu	Glu	Phe	Gln	Arg	Lys	Ile		
						120			125				130				
CTG	AAG	CGA	TCC	GGT	CTC	GGC	GAA	GAG	ACT	TAC	CTC	CCG	GAA	TCT	ATC		488
Leu	Lys	Arg	Ser	Gly	Leu	Gly	Glu	Glu	Thr	Tyr	Leu	Pro	Glu	Ser	Ile		
						135			140				145				
CAC	TGC	ATC	CCG	CCG	CGT	CCG	ACT	ATG	GCG	GCG	GCG	CGT	GAG	GAA	TCG		536
His	Cys	Ile	Pro	Pro	Arg	Pro	Thr	Met	Ala	Ala	Ala	Arg	Glu	Glu	Ser		
						150			155				160			165	
GAG	CAG	GTA	ATC	TTC	GGT	GCA	CTC	GAC	AAT	CTC	TTC	GAG	AAT	ACC	AAA		584
Glu	Gln	Val	Ile	Phe	Gly	Ala	Leu	Asp	Asn	Leu	Phe	Glu	Asn	Thr	Lys		
						170			175				180				
ATC	GAC	CCT	AGG	GAG	ATT	GGT	GTT	GTG	GTG	GTG	AAC	TGC	AGC	TTG	TTT		632
Ile	Asp	Pro	Arg	Glu	Ile	Gly	Val	Val	Val	Val	Asn	Cys	Ser	Leu	Phe		
						185			190				195				
AAC	CCG	ACG	CCT	TCT	TTA	TCC	GCC	ATG	ATT	GTG	AAC	AAG	TAT	AAG	CTT		680
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu		
						200			205				210				
AGA	GGA	AAC	GTG	AAG	AGC	TTT	AAC	CTC	GGA	GGA	ATG	GGA	TGT	AGG	GCT		728
Arg	Gly	Asn	Val	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Arg	Ala		
						215			220				225				

GGT GTC ATC GCC GTT GAT CTC GCT AAT GAC ATT TTA CAG CTC CAT AGA Gly Val Ile Ala Val Asp Leu Ala Asn Asp Ile Leu Gln Leu His Arg 230 235 240 245	776
AAC ACA TTA GCT CTT GTG GTT AGC ACA GAG AAC ATC ACT CAG AAT TGG Asn Thr Leu Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp 250 255 260	824
TAC TTT GGT AAC AAC AAA GCA ATG TTG ATT CCT AAT TGC TTG TTT AGG Tyr Phe Gly Asn Asn Lys Ala Met Leu Ile Pro Asn Cys Leu Phe Arg 265 270 275	872
GTT GGT GGA TCC GCG GTT CTG CTT TCG AAC AAG CCT CGT GAT CGA AAA Val Gly Gly Ser Ala Val Leu Leu Ser Asn Lys Pro Arg Asp Arg Lys 280 285 290	920
CGA TCC AAG TAT AAA CTT GTT CAC ACG GTA CGG ACT CAT AAA GGA TCT Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Lys Gly Ser 295 300 305	968
GAT GAG AAA GCA TTC AAC TGT GTG TAC CAA GAA CAA GAC GAG GAC TTG Asp Glu Lys Ala Phe Asn Cys Val Tyr Gln Glu Gln Asp Glu Asp Leu 310 315 320 325	1016
AAA ACC GGA GTT TCT TTG TCT AAA GAC CTA ATG TCT ATA GCT GGA GAA Lys Thr Gly Val Ser Leu Ser Lys Asp Leu Met Ser Ile Ala Gly Glu 330 335 340	1064
GCT CTA AAG ACA AAT ATC ACC ACT TTG GGT CCT CTG GTT CTT CCA ATA Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Ile 345 350 355	1112
AGC GAG CAG ATT CTG TTC ATT GCG ACT TTT GTT GCA AAG AGA TTG TTC Ser Glu Gln Ile Leu Phe Ile Ala Thr Phe Val Ala Lys Arg Leu Phe 360 365 370	1160
AGT GCC AAG AAG AAG AAG AAG CCT TAC ATA CCG GAT TTC AAG CTT Ser Ala Lys Lys Lys Lys Pro Tyr Ile Pro Asp Phe Lys Leu 375 380 385	1208
GCC TTT GAT CAT TTC TGT ATT CAC GCA GGA GGT AGA GCC GTG ATC GAT Ala Phe Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp 390 395 400 405	1256

GAA CTA GAG AAG AGT TTA AAG CTA TTG CCA AAA CAT GTG GAG GCT TCT		1304
Glu Leu Glu Lys Ser Leu Lys Leu Pro Lys His Val Glu Ala Ser		
410	415	420
AGA ATG ACA TTG CAT AGA TTT GGA AAC ACT TCA TCG AGC TCT ATT TGG		1352
Arg Met Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp		
425	430	435
TAT GAA TTA GCT TAC ACA GAA GCT AAA GGA AGA ATG AGA AAA GGG AAT		1400
Tyr Glu Leu Ala Tyr Thr Glu Ala Lys Gly Arg Met Arg Lys Gly Asn		
440	445	450
CGA GTT TGG CAG ATT GCT TTT GGA AGC GGC TTT AAG TGT AAC AGC GCG		1448
Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala		
455	460	465
GTT TGG GTG GCT CTT CGT GAT GTC GAG CCC TCG GTT AAC AAT CCT TGG		1496
Val Trp Val Ala Leu Arg Asp Val Glu Pro Ser Val Asn Asn Pro Trp		
470	475	480
485		
GAA CAT TGC ATC CAT AGA TAT CCG GTT AAG ATC GAT CTC TGATTCAGC		1545
Glu His Cys Ile His Arg Tyr Pro Val Lys Ile Asp Leu		
490	495	
TTAACCGGTA AAATTGGTCT GTACATATAT TTACCACTGA GTAAAGACAT CAGTTAATGA		1605
TTTGTTGTTA CTCAATTGGG CTAAGTGTAT TATTATATGT GTTGTATATA ATAAAGGTAG		1665
AACGTAAATT TACTAAGAAA AAAAAAAA AAAAAAAA		1704

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CA ATG ACG TCT GTG AAC GTA AAA CTC CTT TAC CAT TAC GTC ATA ACC Met Thr Ser Val Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr 1 5 10 15	47
AAC TTT TTC AAC CTC TGT TTC CCA CTG ACG GGG ATC CTC GCC GGA Asn Phe Phe Asn Leu Cys Phe Phe Pro Leu Thr Gly Ile Leu Ala Gly 20 25 30	95
AAA GGC TCT CGT CTT ACC ACA AAC GAT CTC CAC CAC TTC TAT TCA TAT Lys Gly Ser Arg Leu Thr Thr Asn Asp Leu His His Phe Tyr Ser Tyr 35 40 45	143
CTC CAA CAC AAN CTT ATA ACC TTA ACC CTA CTC TTT GGC TTC ACC GTT Leu Gln His Xxx Leu Ile Thr Leu Thr Leu Leu Phe Gly Phe Thr Val 50 55 60	191
TTT GGT TCG GTT CTC TAC TTC GTA ANC CGA CCC AAA CCG GTT TAC CTC Phe Gly Ser Val Leu Tyr Phe Val Xxx Arg Pro Lys Pro Val Tyr Leu 65 70 75	239
GTT GAC TAC TCC TGC TAC CTT CCA CCA CAA CAT CTT AGC GCT GGT ATC Val Asp Tyr Ser Cys Tyr Leu Pro Pro Gln His Leu Ser Ala Gly Ile 80 85 90 95	287
TCT AAG ACC ATG GAA ATC TTT TAT CAA ATA AGA AAA TCT GAT CCT TTA Ser Lys Thr Met Glu Ile Phe Tyr Gln Ile Arg Lys Ser Asp Pro Leu 100 105 110	335
CGA AAC GTG GCA TTA GAT GAT TCG TCT TCT CTT GAT TTC TTG AGA AAG Arg Asn Val Ala Leu Asp Asp Ser Ser Ser Leu Asp Phe Leu Arg Lys 115 120 125	383
ATT CAA GAG CGT TCA GGT CTA GGC GAT GAA ACC TAC GGC CCC GAG GGA Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Gly Pro Glu Gly 130 135 140	431
CTG TTT GAG ATT CCT CCG AGG AAG AAT TTA GCG TCG GCG CGT GAA GAG Leu Phe Glu Ile Pro Pro Arg Lys Asn Leu Ala Ser Ala Arg Glu Glu 145 150 155	479

ACG GAG CAA GTA ATC AAC GGT GCG CTA AAA AAT CTA TTC GAG AAC AAC	527
Thr Glu Gln Val Ile Asn Gly Ala Leu Lys Asn Leu Phe Glu Asn Asn	
160 165 170 175	
AAA GTT AAC CCT AAA GAG ATT GGT ATA CTT GTG GTG AAC TCA AGC ATG	575
Lys Val Asn Pro Lys Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
TTT AAT CCG ACT CCT TCG TTA TCC GCG ATG GTA GTT AAT ACT TCC AAG	623
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Ser Lys	
195 200 205	
CTC CGA AGC AAC ATC AAA AGC TTT AAT CTT GGA GGA ATG GGT TGC AGT	671
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
GCT GGT GTT ATC GCC ATT GAT CTA GCT AAA GAC TTG TTG CAT GTT CAT	719
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235	
AAA AAC ACA TAT GCT CTT GTG GTG AGC ACA GAG AAC ATC ACT CAA AAC	767
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Asn	
240 245 250 255	
ATT TAT ACC GGT GAT AAC AGA TCC ATG ATG GTT TCG AAT TGC TTG TTC	815
Ile Tyr Thr Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
CGT GTC GGT GGG GCA GCG ATT CTG CTC TCC AAC AAG CCG GGG GAT CGA	863
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
AGA CGG TCC AAG TAC AAG CTA GCT CAC ACG GTT CGA ACG CAT ACC GGA	911
Arg Arg Ser Lys Tyr Lys Leu Ala His Thr Val Arg Thr His Thr Gly	
290 295 300	
GCT GAC GAC AAG TCT TTT GGA TGT GTG CGG CAA GAA GAA GAT GAT AGC	949
Ala Asp Asp Lys Ser Phe Gly Cys Val Arg Gln Glu Glu Asp Asp Ser	
305 310 315	
GGT AAA ACC GGA GTT AGT TTG TCA AAA GAC ATA ACC GTT GTT GCC GGG	1007
Gly Lys Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Val Val Ala Gly	
320 325 330 335	

ATA ACG GTT CAG AAA AAC ATA ACA ACA TTG GGT CCG TTG GTT CTT CCT Ile Thr Val Gln Lys Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro	340 345 350	1055
CTG AGC GAA AAA ATC CTT TTT GTC GTT ACA TTC GTA GCC AAG AAA CTA Leu Ser Glu Lys Ile Leu Phe Val Val Thr Phe Val Ala Lys Lys Leu	355 360 365	1103
TTA AAA GAT AAG ATC AAA CAC TAT TAC GTG CCG GAT TTC AAA CTT GCA Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	370 375 380	1151
GTA GAT CAT TTC TGT ATT CAT GCG GGA GGT AGA GCC GTG ATA GAT GTG Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	385 390 395	1199
TTA GAG AAG AAC TTA GGG CTA TCG CCG ATA GAT GTG GAG GCA TCA AGA Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	400 405 410 415	1247
TCA ACA TTA CAT AGA TTT GGG AAT ACA TCG TCT AGT TCA ATT TGG TAT Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	420 425 430	1295
GAA TTA GCA TAC ATA GAG CCA AAA GGA AGG ATG AAG AAA GGT AAT AAA Glu Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys	435 440 445	1343
GCT TGC CAA ATA GCT GGT GGG TCA GGT TTT AAG TGT AAT AGT GCG GTT Ala Cys Gln Ile Ala Gly Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	450 455 460	1391
TGG GTC GCT TTA CGC AAT GTC GAG GCT TCA GCT AAT AGT CCT TGG GAA Trp Val Ala Leu Arg Asn Val Glu Ala Ser Ala Asn Ser Pro Trp Glu	465 470 475	1439
CAT TGC ATT CAC AAA TAT CCG GTT CAA ATG TAT TCT GGT TCA TCA AAG His Cys Ile His Lys Tyr Pro Val Gln Met Tyr Ser Gly Ser Ser Lys	480 485 490 495	1487
TCA GAG ACT CCT GTC CAA AAC GGT CGG TCC TAATTTATGT ATCTCAAATG Ser Glu Thr Pro Val Gln Asn Gly Arg Ser	500	1537

ATGTTGTCCA CTTTCTCTTT TTTTTTTCT TTTTTTAGTT ATAATTAAAT GGTTACGATG 1597

TTTGTCTAG GTCGTTATAA ATAAAGAATA CATGGGTGTT ACTAGTATAA AAAAAAAA 1657

AAAAAAA 1664

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTTTCTTCTT CCCCAACA ATG ACC CAT AAC CAA AAC CAA CCT CAC CGG GCA 51
Met Thr His Asn Gln Asn Gln Pro His Arg Ala
1 5 10

GTT CCG GTT CAC GTT ACA AAC TCC GAT CAA AAC CAA AAC CAA AAC CAA 99
Val Pro Val His Val Thr Asn Ser Asp Gln Asn Gln Asn Gln Asn Gln
15 20 25

AAC AAT CTC CCA AAT TTT CTC TTA TCT GTT CGG CTC AAA TAT GTA AAA 147
Asn Asn Leu Pro Asn Phe Leu Leu Ser Val Arg Leu Lys Tyr Val Lys
30 35 40

CTT GGG TAC CAT TAC CTA ATC TCC AAC GGT CTC TAC ATC CTC CTC CTC 195
Leu Gly Tyr His Tyr Leu Ile Ser Asn Gly Leu Tyr Ile Leu Leu Leu
45 50 55

CCT CTC CTC GGC GGC ACA ATC GTA AAA CTC TCT TCC TTC ACA CTC AAC 243
Pro Leu Leu Gly Gly Thr Ile Val Lys Leu Ser Ser Phe Thr Leu Asn
60 65 70 75

GAA CTC TCT CTC CTC TAC AAC CAC CTC CGT TTT CAT TTC CTC TCC GCC 291
Glu Leu Ser Leu Leu Tyr Asn His Leu Arg Phe His Phe Leu Ser Ala
80 85 90

ACA CTC GCT ACC GGA CTC TTA ATC TCT CTC TCC ACC GCC TAC TTC ACC	339
Thr Leu Ala Thr Gly Leu Leu Ile Ser Leu Ser Thr Ala Tyr Phe Thr	
95 100 105	
ACC CGT CCT CGT CAT GTC TTC CTC CTC GAC TTC TCA TGC TAC AAA CCT	387
Thr Arg Pro Arg His Val Phe Leu Leu Asp Phe Ser Cys Tyr Lys Pro	
110 115 120	
GAC CCT TCC TTA ATA TGC ACT CGT GAA ACA TTC ATG GAC CGA TCT CAA	435
Asp Pro Ser Leu Ile Cys Thr Arg Glu Thr Phe Met Asp Arg Ser Gln	
125 130 135	
CGT GTA GGT ATC TTC ACA GAA GAC AAC CTC GCT TTT CAA CAA AAG ATC	483
Arg Val Gly Ile Phe Thr Glu Asp Asn Leu Ala Phe Gln Gln Lys Ile	
140 145 150 155	
CTC GAA AGA TCC GGT CTT GGG CAG AAA ACT TAC TTC CCT GAA GCT CTT	531
Leu Glu Arg Ser Gly Leu Gly Gln Lys Thr Tyr Phe Pro Glu Ala Leu	
160 165 170	
CTT CGT GTT CCT CCC AAT CCT TGT ATG GAA GAA GCG AGA AAA GAA GCA	579
Leu Arg Val Pro Pro Asn Pro Cys Met Glu Glu Ala Arg Lys Glu Ala	
175 180 185	
GAG ACT GTT ATG TTC GGA GCT ATA GAC TCT GTT CTT GAG AAA ACC GGT	627
Glu Thr Val Met Phe Gly Ala Ile Asp Ser Val Leu Glu Lys Thr Gly	
190 195 200	
GTG AAA CCT AAA GAT ATC GGA ATC CTT GTC GTG AAT TGT AGT TTG TTT	675
Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe	
205 210 215	
AAT CCG ACG CCG TCA CTT TCC GCC ATG ATT GTG AAT AAG TAT AAG CTT	723
Asn Pro Thr Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu	
220 225 230 235	
AGA GGA AAC ATT TTG AGC TAT AAT CTC GGT GGA ATG GGT TGT AGT GCT	771
Arg Gly Asn Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala	
240 245 250	
GGA CTT ATC TCC ATT GAT CTC GCT AAA CAG CTT CTT CAG GTC CAA CCA	819
Gly Leu Ile Ser Ile Asp Leu Ala Lys Gln Leu Leu Gln Val Gln Pro	
255 260 265	

AAC TCA TAC GCA CTA GTG GTG AGC ACA GAG AAC ATA ACC TTA AAC TGG	867
Asn Ser Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp	
270 275 280	
TAC TTA GGC AAC GAC CGA TCA ATG CTT CTC TCT AAC TGC ATC TTC CGT	915
Tyr Leu Gly Asn Asp Arg Ser Met Leu Leu Ser Asn Cys Ile Phe Arg	
285 290 295	
ATG GGA GGA GCC GCC GTA CTT CTC TCA AAC CGT TCC TCC GAT CGC ACC	963
Met Gly Gly Ala Ala Val Leu Leu Ser Asn Arg Ser Ser Asp Arg Thr	
300 305 310 315	
CGT TCA AAA TAT CAG CTC ATC CAC CCC GTC CGT ACC CAC AAA GGA GCC	1011
Arg Ser Lys Tyr Gln Leu Ile His Pro Val Arg Thr His Lys Gly Ala	
320 325 330	
AAC GAC AAC GCA TTT GGC TGC GTT TAC CAA CGA GAA GAC AAC AAC GAA	1059
Asn Asp Asn Ala Phe Gly Cys Val Tyr Gln Arg Glu Asp Asn Asn Glu	
335 340 345	
GAA GAA ACC GCC AAA ATC GGA GTC TCA CTC TCT AAA AAC CTA ATG GCA	1107
Glu Glu Thr Ala Lys Ile Gly Val Ser Leu Ser Lys Asn Leu Met Ala	
350 355 360	
ATA GCC GGA GAA GCT CTC AAG ACA AAC ATA ACA ACA CTC GGA CCA CTA	1155
Ile Ala Gly Glu Ala Leu Lys Thr Asn Ile Thr Thr Leu Gly Pro Leu	
365 370 375	
GTC TTA CCA ATG TCC GAA CAG ATT CTG TTT TTC CCA ACA CTC GTG GCT	1203
Val Leu Pro Met Ser Glu Gln Ile Leu Phe Phe Pro Thr Leu Val Ala	
380 385 390 395	
CGA AAA ATC TTC AAA GTC AAG AAA ATA AAG CCT TAC ATA CCC GAT TTC	1251
Arg Lys Ile Phe Lys Val Lys Ile Lys Pro Tyr Ile Pro Asp Phe	
400 405 410	
AAG CTA GCT TTC GAG CAT TTC TGC ATC CAT GCG GGA GGT AGA GCA GTG	1299
Lys Leu Ala Phe Glu His Phe Cys Ile His Ala Gly Gly Arg Ala Val	
415 420 425	
CTT GAT GAG ATA GAG AAG AAT TTG GAT TTA TCA GAG TGG CAT ATG GAA	1347
Leu Asp Glu Ile Glu Lys Asn Leu Asp Leu Ser Glu Trp His Met Glu	
430 435 440	

CCA TCG AGG ATG ACT TTA AAC CGG TTT GGT AAT ACT TCG AGT AGC TCA Pro Ser Arg Met Thr Leu Asn Arg Phe Gly Asn Thr Ser Ser Ser Ser 445 450 455	1395
CTT TGG TAT GAA CTT GCG TAT AGT GAA GCT AAA GGG AGG ATT AAG AGA Leu Trp Tyr Glu Leu Ala Tyr Ser Glu Ala Lys Gly Arg Ile Lys Arg 460 465 470 475	1443
GGA GAT AGG ACT TGC CAA ATT GCG TTT GGA TCG GGA TTT AAG TGT AAT Gly Asp Arg Thr Cys Gln Ile Ala Phe Gly Ser Gly Phe Lys Cys Asn 480 485 490	1491
AGT GCG GTT TGG AAA GCT TTG AGA ACC ATT GAT CCT ATT GAT GAG AAG Ser Ala Val Trp Lys Ala Leu Arg Thr Ile Asp Pro Ile Asp Glu Lys 495 500 505	1539
AAG AAT CCA TGG AGT GAT GAG ATT CAT GAG TTT CCA GTT TCT GTT CCT Lys Asn Pro Trp Ser Asp Glu Ile His Glu Phe Pro Val Ser Val Pro 510 515 520	1587
AGG ATC ACT CCA GTT ACT TCT AAC TAGTGTTTT TTTTGGGTC CAACTAGGGAA Arg Ile Thr Pro Val Thr Ser Asn 525 530	1641
TAATATTGTTATGGTTTG TTCTTACGTA CGTACTTTAA GTGATTAGT CTAAAAATAA 1701	
ATTGGTTTCA TAAAAAAAAA AAAAAAAA A	1732

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27 :

AAG CTT AAA CTA GTA TAC CAT TAC TTG ATC TCC AAC GCC ATG TAT TTG	48
Lys Leu Lys Leu Val Tyr His Tyr Leu Ile Ser Asn Ala Met Tyr Leu	
1 5 10 15	
TTA ATG GTG CCG CTT CTA GCA GTA GCC TTT GCT CAT CTC TCC ACG TTG	96
Leu Met Val Pro Leu Leu Ala Val Ala Phe Ala His Leu Ser Thr Leu	
20 25 30	
ACG ATT CAA GAT CTG GTT CAT CTT TGG GAA CAG CTT AAG TTC AAT TTA	144
Thr Ile Gln Asp Leu Val His Leu Trp Glu Gln Leu Lys Phe Asn Leu	
35 40 45	
CTG TCA GTA ACT CTC TGC TCG AGC CTT ATG GTG TTT TTA GGG ACT CTG	192
Leu Ser Val Thr Leu Cys Ser Ser Leu Met Val Phe Leu Gly Thr Leu	
50 55 60	
TAT TTC ATG AGC CGA CCG ACG AAG ATT TAC TTG GTG GAT TTC TCT TGT	240
Tyr Phe Met Ser Arg Pro Thr Lys Ile Tyr Leu Val Asp Phe Ser Cys	
65 70 75 80	
TAC AAG CCG GAA AAA GAG CGT ATA TGC ACG AGA GAG ATT TTC TAT GAG	288
Tyr Lys Pro Glu Lys Glu Arg Ile Cys Thr Arg Glu Ile Phe Tyr Glu	
85 90 95	
AGA TCG AAA CTA ACT GGG AAT TTT ACC GAT GAT AAT TTA ACT TTC CAA	336
Arg Ser Lys Leu Thr Gly Asn Phe Thr Asp Asp Asn Leu Thr Phe Gln	
100 105 110	
AAG AAA ATT ATC GAA AGA TCT GGA TTA GGT CAG AAC ACG TAC TTA CCT	384
Lys Lys Ile Ile Glu Arg Ser Gly Leu Gly Gln Asn Thr Tyr Leu Pro	
115 120 125	
GAG GCC GTT CTA CGG GTT CCG CCC AAT CCG TGT ATG GCG GAG GCT AGA	432
Glu Ala Val Leu Arg Val Pro Pro Asn Pro Cys Met Ala Glu Ala Arg	
130 135 140	
AAG GAG GCT GAG ATG GTT ATG TTC GGT GCG ATC GAT GAA TTG TTG GAG	480
Lys Glu Ala Glu Met Val Met Phe Gly Ala Ile Asp Glu Leu Leu Glu	
145 150 155 160	

AAA ACC GGG GTT AAA CCT AAG GAT ATC GGT ATT CTT GTG GTG AAT TGC 528
Lys Thr Gly Val Lys Pro Lys Asp Ile Gly Ile Leu Val Val Asn Cys
165 170 175

AGC TTG TTC AAT CCG ACG CCG TCT CTG TCC GCA ATG GTG GTT AAT CGG 576
Ser Leu Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Arg
180 185 190

TAC AAG CTT AGA GGG AAT ATC ATA AGT TAT AAC CTT GGC GGG ATG G 622
Tyr Lys Leu Arg Gly Asn Ile Ile Ser Tyr Asn Leu Gly Gly Met
195 200 205

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 residues
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28 :

Asn Ile Thr Thr Leu Gly
5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 residues
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29 :

Ser Asn Cys Lys Phe Gly
5

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAUCAUCAUC AUGTCGACAA AATGACGTCC ATTAACGTAA AG

42

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31 :

CUACUACUAC UAGTCGACGG ATCCTATTG GAAGCTTG CATTGTTAG

50

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 residues
- (B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE: Xaa at position 3 = Leu or Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32 :

Lys Leu Xaa Tyr His Tyr
5

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33 :

CAUCAUCAUC AUGAATTCAA GCTTAARYTN BKNTAYCAYT A

41

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 residues

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34 :

Asn Leu Gly Gly Met Gly Cys
5

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35 :

CAUCAUCAUC AUGAATTCAA GCTTAAYYTN GGNNGNATGG G

41

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

- (A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36 :

CUACUACUAC UAGGATCCGT CGACCCATNC CNCCNARRTT

40

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 residues
- (B) TYPE: amino acids
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37 :

Gly Phe Lys Cys Asn Ser
5

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38 :

CUACUACUAC UAGGATCCGT CGACSWRTTR CAYTTRAANC C

41

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other

(A) synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39 :

CUACUACUAC UASWRTTRCA YTTRAANCC

29